

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1566	100.0	300	15	US-10-041-018-46	Sequence 46, Appl
2	1550	99.0	304	9	US-09-925-302-614	Sequence 614, App
3	1550	99.0	304	10	US-09-925-302-614	Sequence 614, Appl
4	928	59.3	338	15	US-10-041-018-24	Sequence 24, Appl
5	928	59.3	338	15	US-10-041-018-77	Sequence 77, Appl
6	862.5	55.1	335	15	US-10-041-018-23	Sequence 23, Appl
7	862.5	55.1	335	15	US-10-041-018-76	Sequence 76, Appl
8	806.5	51.5	303	15	US-10-041-018-34	Sequence 34, Appl
9	797.5	50.9	428	15	US-10-369-493-4221	Sequence 4221, Ap
10	792	50.6	348	15	US-10-369-493-12405	Sequence 12405, A
11	725	46.3	452	15	US-10-369-493-12982	Sequence 12982, A
12	707	45.1	376	15	US-10-001-192A-15	Sequence 15, Appl
13	613.5	39.2	319	15	US-10-369-493-12991	Sequence 12991, A

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1566	100.0	300	1	GGPP_HUMAN	O95749 h geranylge	
2	1558	99.5	300	2	Q6NW19	Q6nw19 homo sapien	
3	1516	96.8	294	1	GGPP_BOVIN	P56966 b geranylge	
4	1490	95.1	300	2	Q6F596	Q6f596 rattus norv	
5	1476	94.3	300	1	GGPP_MOUSE	Q9wtn0 m geranylge	
6	1322	84.4	327	2	Q7ZTY0	Q7zty0 brachydanio	
7	1163	74.3	236	2	Q9CZZ6	Q9czz6 mus musculu	
8	928	59.3	338	2	O61539	O61539 drosophila	
9	928	59.3	338	2	Q9VS54	Q9vs54 drosophila	
10	888	56.7	357	2	Q7QII9	Q7qii9 anopheles g	
11	862.5	55.1	335	2	O61538	O61538 drosophila	
12	819	52.3	335	2	Q86F69	Q86f69 schistosoma	
13	806.5	51.5	303	2	Q9P885	Q9p885 mucor circi	
14	802	51.2	340	2	Q672V6	Q672v6 aspergillus	
15	797.5	50.9	428	1	GGPP_NEUCR	P24322 n geranylge	
16	794.5	50.7	396	2	Q874I1	Q874i1 emericella	
17	794	50.7	375	2	Q9C452	Q9c452 penicillium	

Database : A_Geneseq_16Dec04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		Length	DB	ID	Description
	Score	% Match				
1	1566	100.0	300	3	AAy68909	Aay68909 A geranyl
2	1566	100.0	300	8	ADJ10383	Adj10383 Human ger
3	1566	100.0	300	8	ADM98626	Adm98626 Geranylge
4	1550	99.0	304	3	AAB58276	Aab58276 Lung canc
5	1523	97.3	300	2	AAW59753	Aaw59753 Human ger
6	1523	97.3	300	2	AAy27005	Aay27005 Human ger
7	1519	97.0	300	2	AAR97565	Aar97565 Human ger
8	1244.5	79.5	320	4	AAU30743	Aau30743 Novel hum
9	928	59.3	338	4	ABB60947	Abb60947 Drosophil
10	928	59.3	338	8	ADM98657	Adm98657 Geranylge
11	928	59.3	338	8	ADM98604	Adm98604 Geranylge
12	862.5	55.1	335	8	ADM98656	Adm98656 Geranylge
13	862.5	55.1	335	8	ADM98603	Adm98603 Geranylge

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	1523	97.3		300	1	US-08-469-665-2	Sequence 2, Appli
2	1523	97.3		300	2	US-09-038-596-2	Sequence 2, Appli
3	1523	97.3		300	5	PCT-US95-00421-2	Sequence 2, Appli
4	707	45.1		376	3	US-09-091-725-15	Sequence 15, Appl
5	583	37.2		335	2	US-08-761-344-2	Sequence 2, Appli
6	238.5	15.2		341	4	US-09-252-991A-21448	Sequence 21448, A
7	229.5	14.7		340	4	US-09-543-681A-5778	Sequence 5778, Ap
8	225.5	14.4		162	4	US-09-248-796A-17986	Sequence 17986, A
9	213.5	13.6		165	4	US-09-248-796A-17985	Sequence 17985, A
10	207	13.2		330	1	US-08-410-167A-4	Sequence 4, Appli
11	207	13.2		330	2	US-08-898-560-1	Sequence 1, Appli
12	206	13.2		330	3	US-09-101-126-1	Sequence 1, Appli
13	197.5	12.6		342	4	US-09-489-039A-13653	Sequence 13653, A
14	197	12.6		353	4	US-09-328-352-4226	Sequence 4226, Ap